



Sequence Listing

<110> Kainoh, Mie
Tanaka, Toshiaki
<120> Chimeric proteins, their heterodimer complexes, and platelet
substitutes
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<150> PCT/JP98/00370
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Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
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cctaaccag gccctgcaca caaaggggca ggtgctgggc tcagacctgc caagagccat	3645
atccgggagg accctgcccc tgacctaacg ccacccaaa ggccaaactc tccactccct	3705
cagctcggac accttctctc ctcccagatt ccagtaactc ccaatcttct ctctgca	3762
gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca	3807
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro	
1110 1115 1120	
ggtaagccag cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc	3867
tgcattccagg gacaggcccc agccgggtgc tgacacgtcc acctccatct ctctctca	3925
gca cct gaa ctg ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa	3973
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys	
1125 1130 1135	
ccc aag gac acc ctg atg atc tcc egg acc cct gag gtc aca tgc gtg	4021
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val	
1140 1145 1150	
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac	4069
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr	
1155 1160 1165	
gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag	4117
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu	
1170 1175 1180 1185	
cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac	4165
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His	
1190 1195 1200	
cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa	4213
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys	
1205 1210 1215	
gcc ctg cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa	4255
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys	
1220 1225 1230	
ggtagggacc gtgggggtgc agggccacat ggacagaggc cggtcggcc caccctctgc	4315
cctgagagt accgctgtac caacctctgt cctaca ggg cag ccc cga gaa cca	4369
Gly Gln Pro Arg Glu Pro	

1235
 cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag 4417
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 1240 1245 1250
 gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc 4465
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 1255 1260 1265
 gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg 4513
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 1270 1275 1280 1285
 cct ccc gtg ctg gat tcc gac ggc tcc ttc ttc ctc tac agc aag ctc 4561
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 1290 1295 1300
 acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc 4609
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 1305 1310 1315
 gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc 4657
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 1320 1325 1330
 ctg tct ccg ggt aaa tga 4675
 Leu Ser Pro Gly Lys
 1335

<210> 20
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> Synthetic DNA
 <223> Oligonucleotide
 <400> 20
 gctcgagcaa acccagcgca actacgg 27

<210> 21
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 <213> Artificial Sequence
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 <223> Oligonucleotide
 <400> 21

atagtgcctt gatgaccatt g 21

<210> 22
 <211> 22
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 <223> Oligonucleotide
 <400> 22
 gatggcttta atgatgtgat tg 22

<210> 23
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<223> Oligonucleotide
<400> 23
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<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence
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<223> Synthetic peptide
Circular
<400> 24

Cys Ile Pro Glu Leu Ile Val Cys
1 5

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence
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Circular
<400> 25

Cys Met Arg Tyr Thr Ser Ala Cys
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence
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<223> Synthetic peptide
Circular
<400> 26

Cys Glu Trp Met Lys Arg Phe Cys
1 5

<210> 27
<211> 8
<212> PRT
<213> Artificial Sequence
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<223> Synthetic peptide
Circular
<400> 27

Cys Tyr Thr Thr Arg Leu Lys Cys
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence
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<223> Synthetic peptide
Circular
<400> 28
Cys Leu Arg Tyr Ser Val Pro Cys
1 5

<210> 29
<211> 8
<212> PRT
<213> Artificial Sequence
<220> Peptide
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Circular
<400> 29
Cys Ile Val Asn Arg Leu Gly Cys
1 5

<210> 30
<211> 8
<212> PRT
<213> Artificial Sequence
<220> Peptide

<223> Synthetic peptide
Circular
<400> 30
Cys Gly Leu Gln Ala Leu Pro Cys
1 5

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence
<220> Peptide

<223> Synthetic peptide
Circular

<400> 31
Cys Lys Leu Lys Gly Thr Met Cys
1 5

<210> 32
<211> 1179
<212> PRT
<213> Homo sapien

<400> 32

Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
-35 -30 -25

Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
-20 -15 -10

Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
-5 1 5

Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
10 15 20 25

His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
30 35 40

Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
45 50 55

Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
60 65 70

Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
75 80 85

Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
90 95 100 105

Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
110 115 120

Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
125 130 135

Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
140 145 150

Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
155 160 165

Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
170 175 180 185

Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
190 195 200

Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
205 210 215

Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
220 225 230

Glu	Val	Val	Gly	Gly	Ala	Pro	Gln	His	Glu	Gln	Ile	Gly	Lys	Ala	Tyr	235	240	245
Ile	Phe	Ser	Ile	Asp	Glu	Lys	Glu	Leu	Asn	Ile	Leu	His	Glu	Met	Lys	250	255	260
Gly	Lys	Lys	Leu	Gly	Ser	Tyr	Phe	Gly	Ala	Ser	Val	Cys	Ala	Val	Asp	270	275	280
Leu	Asn	Ala	Asp	Gly	Phe	Ser	Asp	Leu	Leu	Val	Gly	Ala	Pro	Met	Gln	285	290	295
Ser	Thr	Ile	Arg	Glu	Glu	Gly	Arg	Val	Phe	Val	Tyr	Ile	Asn	Ser	Gly	300	305	310
Ser	Gly	Ala	Val	Met	Asn	Ala	Met	Glu	Thr	Asn	Leu	Val	Gly	Ser	Asp	315	320	325
Lys	Tyr	Ala	Ala	Arg	Phe	Gly	Glu	Ser	Ile	Val	Asn	Leu	Gly	Asp	Ile	330	335	340
Asp	Asn	Asp	Gly	Phe	Glu	Asp	Val	Ala	Ile	Gly	Ala	Pro	Gln	Glu	Asp	350	355	360
Asp	Leu	Gln	Gly	Ala	Ile	Tyr	Ile	Tyr	Asn	Gly	Arg	Ala	Asp	Gly	Ile	365	370	375
Ser	Ser	Thr	Phe	Ser	Gln	Arg	Ile	Glu	Gly	Leu	Gln	Ile	Ser	Lys	Ser	380	385	390
Leu	Ser	Met	Phe	Gly	Gln	Ser	Ile	Ser	Gly	Gln	Ile	Asp	Ala	Asp	Asn	395	400	405
Asn	Gly	Tyr	Val	Asp	Val	Ala	Val	Gly	Ala	Phe	Arg	Ser	Asp	Ser	Ala	410	415	420
Val	Leu	Leu	Arg	Thr	Arg	Pro	Val	Val	Ile	Val	Asp	Ala	Ser	Leu	Ser	430	435	440
His	Pro	Glu	Ser	Val	Asn	Arg	Thr	Lys	Phe	Asp	Cys	Val	Glu	Asn	Gly	445	450	455
Trp	Pro	Ser	Val	Cys	Ile	Asp	Leu	Thr	Leu	Cys	Phe	Ser	Tyr	Lys	Gly	460	465	470
Lys	Glu	Val	Pro	Gly	Tyr	Ile	Val	Leu	Phe	Tyr	Asn	Met	Ser	Leu	Asp	475	480	485
Val	Asn	Arg	Lys	Ala	Glu	Ser	Pro	Pro	Arg	Phe	Tyr	Phe	Ser	Ser	Asn	490	495	500
Gly	Thr	Ser	Asp	Val	Ile	Thr	Gly	Ser	Ile	Gln	Val	Ser	Ser	Arg	Glu	510	515	520

Ala	Asn	Cys	Arg	Thr	His	Gln	Ala	Phe	Met	Arg	Lys	Asp	Val	Arg	Asp		
			525					530					535				
Ile	Leu	Thr	Pro	Ile	Gln	Ile	Glu	Ala	Ala	Tyr	His	Leu	Gly	Pro	His		
		540					545					550					
Val	Ile	Ser	Lys	Arg	Ser	Thr	Glu	Glu	Phe	Pro	Pro	Leu	Gln	Pro	Ile		
	555					560					565						
Leu	Gln	Gln	Lys	Lys	Glu	Lys	Asp	Ile	Met	Lys	Lys	Thr	Ile	Asn	Phe		
570					575					580					585		
Ala	Arg	Phe	Cys	Ala	His	Glu	Asn	Cys	Ser	Ala	Asp	Leu	Gln	Val	Ser		
				590					595					600			
Ala	Lys	Ile	Gly	Phe	Leu	Lys	Pro	His	Glu	Asn	Lys	Thr	Tyr	Leu	Ala		
			605					610					615				
Val	Gly	Ser	Met	Lys	Thr	Leu	Met	Leu	Asn	Val	Ser	Leu	Phe	Asn	Ala		
		620					625					630					
Gly	Asp	Asp	Ala	Tyr	Glu	Thr	Thr	Leu	His	Val	Lys	Leu	Pro	Val	Gly		
	635					640					645						
Leu	Tyr	Phe	Ile	Lys	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Gln	Ile	Asn	Cys		
650					655				660						665		
Glu	Val	Thr	Asp	Asn	Ser	Gly	Val	Val	Gln	Leu	Asp	Cys	Ser	Ile	Gly		
				670					675					680			
Tyr	Ile	Tyr	Val	Asp	His	Leu	Ser	Arg	Ile	Asp	Ile	Ser	Phe	Leu	Leu		
			685					690					695				
Asp	Val	Ser	Ser	Leu	Ser	Arg	Ala	Glu	Glu	Asp	Leu	Ser	Ile	Thr	Val		
		700					705					710					
His	Ala	Thr	Cys	Glu	Asn	Glu	Glu	Glu	Met	Asp	Asn	Leu	Lys	His	Ser		
	715					720					725						
Arg	Val	Thr	Val	Ala	Ile	Pro	Leu	Lys	Tyr	Glu	Val	Lys	Leu	Thr	Val		
730					735					740					745		
His	Gly	Phe	Val	Asn	Pro	Thr	Ser	Phe	Val	Tyr	Gly	Ser	Asn	Asp	Glu		
				750					755					760			
Asn	Glu	Pro	Glu	Thr	Cys	Met	Val	Glu	Lys	Met	Asn	Leu	Thr	Phe	His		
			765					770					775				
Val	Ile	Asn	Thr	Gly	Asn	Ser	Met	Ala	Pro	Asn	Val	Ser	Val	Glu	Ile		
		780					785					790					
Met	Val	Pro	Asn	Ser	Phe	Ser	Pro	Gln	Thr	Asp	Lys	Leu	Phe	Asn	Ile		
						800					805						

Leu Asp Val Gln Thr Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln
 810 815 820 825

Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys
 830 835 840

Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
 845 850 855

Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
 860 865 870

Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
 875 880 885

Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
 890 895 900 905

Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn
 910 915 920

Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln
 925 930 935

Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu Glu Pro Lys Ser Cys Asp
 940 945 950

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 955 960 965

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 970 975 980 985

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 990 995 1000

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 1005 1010 1015

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 1020 1025 1030

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 1035 1040 1045

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 1050 1055 1060 1065

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 1070 1075 1080

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 1085 1090 1095

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 1100 1105 1110
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 1115 1120 1125
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 1130 1135 1140 1145
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 1150 1155 1160
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 1165 1170 1175

Gly Lys

<210> 33
 <211> 943
 <212> PRT
 <213> Homo sapien
 <400> 33

Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys
 -20 -15 -10 -5
 Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala
 1 5 10
 Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
 15 20 25
 Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
 30 35 40
 Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile
 45 50 55 60
 Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
 65 70 75
 Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His
 80 85 90
 Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro
 95 100 105
 Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
 110 115 120

Leu	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Tyr	Ser	Met	Lys	Asp	Asp	Leu	Glu	125	130	135				140
Asn	Val	Lys	Ser	Leu	Gly	Thr	Asp	Leu	Met	Asn	Glu	Met	Arg	Arg	Ile		145	150				155
Thr	Ser	Asp	Phe	Arg	Ile	Gly	Phe	Gly	Ser	Phe	Val	Glu	Lys	Thr	Val		160	165				170
Met	Pro	Tyr	Ile	Ser	Thr	Thr	Pro	Ala	Lys	Leu	Arg	Asn	Pro	Cys	Thr		175	180				185
Ser	Glu	Gln	Asn	Cys	Thr	Thr	Pro	Phe	Ser	Tyr	Lys	Asn	Val	Leu	Ser		190	195				200
Leu	Thr	Asn	Lys	Gly	Glu	Val	Phe	Asn	Glu	Leu	Val	Gly	Lys	Gln	Arg	205	210	215				220
Ile	Ser	Gly	Asn	Leu	Asp	Ser	Pro	Glu	Gly	Gly	Phe	Asp	Ala	Ile	Met		225	230				235
Gln	Val	Ala	Val	Cys	Gly	Ser	Leu	Ile	Gly	Trp	Arg	Asn	Val	Thr	Arg		240	245				250
Leu	Leu	Val	Phe	Ser	Thr	Asp	Ala	Gly	Phe	His	Phe	Ala	Gly	Asp	Gly		255	260				265
Lys	Leu	Gly	Gly	Ile	Val	Leu	Pro	Asn	Asp	Gly	Gln	Cys	His	Leu	Glu	270	275	280				
Asn	Asn	Met	Tyr	Thr	Met	Ser	His	Tyr	Tyr	Asp	Tyr	Pro	Ser	Ile	Ala	285	290	295				300
His	Leu	Val	Gln	Lys	Leu	Ser	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Phe	Ala		305	310				315
Val	Thr	Glu	Glu	Phe	Gln	Pro	Val	Tyr	Lys	Glu	Leu	Lys	Asn	Leu	Ile		320	325				330
Pro	Lys	Ser	Ala	Val	Gly	Thr	Leu	Ser	Ala	Asn	Ser	Ser	Asn	Val	Ile		335	340				345
Gln	Leu	Ile	Ile	Asp	Ala	Tyr	Asn	Ser	Leu	Ser	Ser	Glu	Val	Ile	Leu	350	355	360				
Glu	Asn	Gly	Lys	Leu	Ser	Glu	Gly	Val	Thr	Ile	Ser	Tyr	Lys	Ser	Tyr	365	370	375				380
Cys	Lys	Asn	Gly	Val	Asn	Gly	Thr	Gly	Glu	Asn	Gly	Arg	Lys	Cys	Ser		385	390				395
Asn	Ile	Ser	Ile	Gly	Asp	Glu	Val	Gln	Phe	Glu	Ile	Ser	Ile	Thr	Ser		400	405				410

Asn	Lys	Cys	Pro	Lys	Lys	Asp	Ser	Asp	Ser	Phe	Lys	Ile	Arg	Pro	Leu	415	420	425
Gly	Phe	Thr	Glu	Glu	Val	Glu	Val	Ile	Leu	Gln	Tyr	Ile	Cys	Glu	Cys	430	435	440
Glu	Cys	Gln	Ser	Glu	Gly	Ile	Pro	Glu	Ser	Pro	Lys	Cys	His	Glu	Gly	445	450	455
Asn	Gly	Thr	Phe	Glu	Cys	Gly	Ala	Cys	Arg	Cys	Asn	Glu	Gly	Arg	Val	465	470	475
Gly	Arg	His	Cys	Glu	Cys	Ser	Thr	Asp	Glu	Val	Asn	Ser	Glu	Asp	Met	480	485	490
Asp	Ala	Tyr	Cys	Arg	Lys	Glu	Asn	Ser	Ser	Glu	Ile	Cys	Ser	Asn	Asn	495	500	505
Gly	Glu	Cys	Val	Cys	Gly	Gln	Cys	Val	Cys	Arg	Lys	Arg	Asp	Asn	Thr	510	515	520
Asn	Glu	Ile	Tyr	Ser	Gly	Lys	Phe	Cys	Glu	Cys	Asp	Asn	Phe	Asn	Cys	525	530	535
Asp	Arg	Ser	Asn	Gly	Leu	Ile	Cys	Gly	Gly	Asn	Gly	Val	Cys	Lys	Cys	545	550	555
Arg	Val	Cys	Glu	Cys	Asn	Pro	Asn	Tyr	Thr	Gly	Ser	Ala	Cys	Asp	Cys	560	565	570
Ser	Leu	Asp	Thr	Ser	Thr	Cys	Glu	Ala	Ser	Asn	Gly	Gln	Ile	Cys	Asn	575	580	585
Gly	Arg	Gly	Ile	Cys	Glu	Cys	Gly	Val	Cys	Lys	Cys	Thr	Asp	Pro	Lys	590	595	600
Phe	Gln	Gly	Gln	Thr	Cys	Glu	Met	Cys	Gln	Thr	Cys	Leu	Gly	Val	Cys	605	610	615
Ala	Glu	His	Lys	Glu	Cys	Val	Gln	Cys	Arg	Ala	Phe	Asn	Lys	Gly	Glu	625	630	635
Lys	Lys	Asp	Thr	Cys	Thr	Gln	Glu	Cys	Ser	Tyr	Phe	Asn	Ile	Thr	Lys	640	645	650
Val	Glu	Ser	Arg	Asp	Lys	Leu	Pro	Gln	Pro	Val	Gln	Pro	Asp	Pro	Val	655	660	665
Ser	His	Cys	Lys	Glu	Lys	Asp	Val	Asp	Asp	Cys	Trp	Phe	Tyr	Phe	Thr	670	675	680
Tyr	Ser	Val	Asn	Gly	Asn	Asn	Glu	Val	Met	Val	His	Val	Val	Glu	Asn	685	690	695
																		700

Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu Glu Pro Lys Ser Cys
 705 710 715
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 720 725 730
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 735 740 745
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 750 755 760
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 765 770 775 780
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 785 790 795
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 800 805 810
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 815 820 825
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 830 835 840
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 845 850 855 860
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 865 870 875
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 880 885 890
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 895 900 905
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 910 915 920
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 925 930 935 940

Pro Gly Lys

<210> 34

<211> 1338

<212> PRT

<213> Homo sapien

<300>

<400> 34

Met	Gly	Pro	Glu	Arg	Thr	Gly	Ala	Ala	Pro	Leu	Pro	Leu	Leu	Leu	Val	-25	-20	-15
Leu	Ala	Leu	Ser	Gln	Gly	Ile	Leu	Asn	Cys	Cys	Leu	Ala	Tyr	Asn	Val	-10	-5	1
Gly	Leu	Pro	Glu	Ala	Lys	Ile	Phe	Ser	Gly	Pro	Ser	Ser	Glu	Gln	Phe	5	10	15
Gly	Tyr	Ala	Val	Gln	Gln	Phe	Ile	Asn	Pro	Lys	Gly	Asn	Trp	Leu	Leu	20	25	30
Val	Gly	Ser	Pro	Trp	Ser	Gly	Phe	Pro	Glu	Asn	Arg	Met	Gly	Asp	Val	40	45	50
Tyr	Lys	Cys	Pro	Val	Asp	Leu	Ser	Thr	Ala	Thr	Cys	Glu	Lys	Leu	Asn	55	60	65
Leu	Gln	Thr	Ser	Thr	Ser	Ile	Pro	Asn	Val	Thr	Glu	Met	Lys	Thr	Asn	70	75	80
Met	Ser	Leu	Gly	Leu	Ile	Leu	Thr	Arg	Asn	Met	Gly	Thr	Gly	Gly	Phe	85	90	95
Leu	Thr	Cys	Gly	Pro	Leu	Trp	Ala	Gln	Gln	Cys	Gly	Asn	Gln	Tyr	Tyr	100	105	110
Thr	Thr	Gly	Val	Cys	Ser	Asp	Ile	Ser	Pro	Asp	Phe	Gln	Leu	Ser	Ala	120	125	130
Ser	Phe	Ser	Pro	Ala	Thr	Gln	Pro	Cys	Pro	Ser	Leu	Ile	Asp	Val	Val	135	140	145
Val	Val	Cys	Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys	150	155	160
Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys	165	170	175
Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe	180	185	190
Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser	200	205	210
Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile	215	220	225
Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg	230	235	240
Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	245	250	255

Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile	260	265	270	275
Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu	280	285	290	
Asp	Thr	Lys	Asn	Leu	Ile	Lys	Glu	Ile	Lys	Ala	Ile	Ala	Ser	Ile	Pro	295	300	305	
Thr	Glu	Arg	Tyr	Phe	Phe	Asn	Val	Ser	Asp	Glu	Ala	Ala	Leu	Leu	Glu	310	315	320	
Lys	Ala	Gly	Thr	Leu	Gly	Glu	Gln	Ile	Phe	Ser	Ile	Glu	Gly	Thr	Val	325	330	335	
Gln	Gly	Gly	Asp	Asn	Phe	Gln	Met	Glu	Met	Ser	Gln	Val	Gly	Phe	Ser	340	345	350	355
Ala	Asp	Tyr	Ser	Ser	Gln	Asn	Asp	Ile	Leu	Met	Leu	Gly	Ala	Val	Gly	360	365	370	
Ala	Phe	Gly	Trp	Ser	Gly	Thr	Ile	Val	Gln	Lys	Thr	Ser	His	Gly	His	375	380	385	
Leu	Ile	Phe	Pro	Lys	Gln	Ala	Phe	Asp	Gln	Ile	Leu	Gln	Asp	Arg	Asn	390	395	400	
His	Ser	Ser	Tyr	Leu	Gly	Tyr	Ser	Val	Ala	Ala	Ile	Ser	Thr	Gly	Glu	405	410	415	
Ser	Thr	His	Phe	Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	Tyr	Thr	Gly	Gln	420	425	430	435
Ile	Val	Leu	Tyr	Ser	Val	Asn	Glu	Asn	Gly	Asn	Ile	Thr	Val	Ile	Gln	440	445	450	
Ala	His	Arg	Gly	Asp	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ser	Val	Leu	Cys	455	460	465	
Ser	Val	Asp	Val	Asp	Lys	Asp	Thr	Ile	Thr	Asp	Val	Leu	Leu	Val	Gly	470	475	480	
Ala	Pro	Met	Tyr	Met	Ser	Asp	Leu	Lys	Lys	Glu	Glu	Gly	Arg	Val	Tyr	485	490	495	
Leu	Phe	Thr	Ile	Lys	Lys	Gly	Ile	Leu	Gly	Gln	His	Gln	Phe	Leu	Glu	500	505	510	515
Gly	Pro	Glu	Gly	Ile	Glu	Asn	Thr	Arg	Phe	Gly	Ser	Ala	Ile	Ala	Ala	520	525	530	
Leu	Ser	Asp	Ile	Asn	Met	Asp	Gly	Phe	Asn	Asp	Val	Ile	Val	Gly	Ser	535	540	545	

Pro	Leu	Glu	Asn	Gln	Asn	Ser	Gly	Ala	Val	Tyr	Ile	Tyr	Asn	Gly	His	550	555	560
Gln	Gly	Thr	Ile	Arg	Thr	Lys	Tyr	Ser	Gln	Lys	Ile	Leu	Gly	Ser	Asp	565	570	575
Gly	Ala	Phe	Arg	Ser	His	Leu	Gln	Tyr	Phe	Gly	Arg	Ser	Leu	Asp	Gly	580	585	590
Tyr	Gly	Asp	Leu	Asn	Gly	Asp	Ser	Ile	Thr	Asp	Val	Ser	Ile	Gly	Ala	600	605	610
Phe	Gly	Gln	Val	Val	Gln	Leu	Trp	Ser	Gln	Ser	Ile	Ala	Asp	Val	Ala	615	620	625
Ile	Glu	Ala	Ser	Phe	Thr	Pro	Glu	Lys	Ile	Thr	Leu	Val	Asn	Lys	Asn	630	635	640
Ala	Gln	Ile	Ile	Leu	Lys	Leu	Cys	Phe	Ser	Ala	Lys	Phe	Arg	Pro	Thr	645	650	655
Lys	Gln	Asn	Asn	Gln	Val	Ala	Ile	Val	Tyr	Asn	Ile	Thr	Leu	Asp	Ala	660	665	670
Asp	Gly	Phe	Ser	Ser	Arg	Val	Thr	Ser	Arg	Gly	Leu	Phe	Lys	Glu	Asn	680	685	690
Asn	Glu	Arg	Cys	Leu	Gln	Lys	Asn	Met	Val	Val	Asn	Gln	Ala	Gln	Ser	695	700	705
Cys	Pro	Glu	His	Ile	Ile	Tyr	Ile	Gln	Glu	Pro	Ser	Asp	Val	Val	Asn	710	715	720
Ser	Leu	Asp	Leu	Arg	Val	Asp	Ile	Ser	Leu	Glu	Asn	Pro	Gly	Thr	Ser	725	730	735
Pro	Ala	Leu	Glu	Ala	Tyr	Ser	Glu	Thr	Ala	Lys	Val	Phe	Ser	Ile	Pro	740	745	750
Phe	His	Lys	Asp	Cys	Gly	Glu	Asp	Gly	Leu	Cys	Ile	Ser	Asp	Leu	Val	760	765	770
Leu	Asp	Val	Arg	Gln	Ile	Pro	Ala	Ala	Gln	Glu	Gln	Pro	Phe	Ile	Val	775	780	785
Ser	Asn	Gln	Asn	Lys	Arg	Leu	Thr	Phe	Ser	Val	Thr	Leu	Lys	Asn	Lys	790	795	800
Arg	Glu	Ser	Ala	Tyr	Asn	Thr	Gly	Ile	Val	Val	Asp	Phe	Ser	Glu	Asn	805	810	815
Leu	Phe	Phe	Ala	Ser	Phe	Ser	Leu	Pro	Val	Asp	Gly	Thr	Glu	Val	Thr	820	825	830

Cys	Gln	Val	Ala	Ala	Ser	Gln	Lys	Ser	Val	Ala	Cys	Asp	Val	Gly	Tyr		
				840					845					850			
Pro	Ala	Leu	Lys	Arg	Glu	Gln	Gln	Val	Thr	Phe	Thr	Ile	Asn	Phe	Asp		
			855					860					865				
Phe	Asn	Leu	Gln	Asn	Leu	Gln	Asn	Gln	Ala	Ser	Leu	Ser	Phe	Gln	Ala		
		870					875					880					
Leu	Ser	Glu	Ser	Gln	Glu	Glu	Asn	Lys	Ala	Asp	Asn	Leu	Val	Asn	Leu		
	885					890					895						
Lys	Ile	Pro	Leu	Leu	Tyr	Asp	Ala	Glu	Ile	His	Leu	Thr	Arg	Ser	Thr		
900					905					910					915		
Asn	Ile	Asn	Phe	Tyr	Glu	Ile	Ser	Ser	Asp	Gly	Asn	Val	Pro	Ser	Ile		
				920					925					930			
Val	His	Ser	Phe	Glu	Asp	Val	Gly	Pro	Lys	Phe	Ile	Phe	Ser	Leu	Lys		
			935					940					945				
Val	Thr	Thr	Gly	Ser	Val	Pro	Val	Ser	Met	Ala	Thr	Val	Ile	Ile	His		
		950					955					960					
Ile	Pro	Gln	Tyr	Thr	Lys	Glu	Lys	Asn	Pro	Leu	Met	Tyr	Leu	Thr	Gly		
	965					970					975						
Val	Gln	Thr	Asp	Lys	Ala	Gly	Asp	Ile	Ser	Cys	Asn	Ala	Asp	Ile	Asn		
980					985					990					995		
Pro	Leu	Lys	Ile	Gly	Gln	Thr	Ser	Ser	Ser	Val	Ser	Phe	Lys	Ser	Glu		
				1000					1005					1010			
Asn	Phe	Arg	His	Thr	Lys	Glu	Leu	Asn	Cys	Arg	Thr	Ala	Ser	Cys	Ser		
		1015						1020					1025				
Asn	Val	Thr	Cys	Trp	Leu	Lys	Asp	Val	His	Met	Lys	Gly	Glu	Tyr	Phe		
	1030						1035					1040					
Val	Asn	Val	Thr	Thr	Arg	Ile	Trp	Asn	Gly	Thr	Phe	Ala	Ser	Ser	Thr		
	1045					1050				1055							
Phe	Gln	Thr	Val	Gln	Leu	Thr	Ala	Ala	Ala	Glu	Ile	Asn	Thr	Tyr	Asn		
1060					1065					1070					1075		
Pro	Glu	Ile	Tyr	Val	Ile	Glu	Asp	Asn	Thr	Val	Thr	Ile	Pro	Leu	Met		
			1080						1085					1090			
Ile	Met	Lys	Pro	Asp	Glu	Lys	Ala	Glu	Val	Pro	Thr	Asp	Pro	Glu	Glu		
		1095						1100					1105				
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro		
	1110						1115					1120					

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
1125 1130 1135

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
1140 1145 1150 1155

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
1160 1165 1170

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
1175 1180 1185

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
1190 1195 1200

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
1205 1210 1215

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
1220 1225 1230 1235

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
1240 1245 1250

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
1255 1260 1265

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
1270 1275 1280

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
1285 1290 1295

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
1300 1305 1310 1315

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
1320 1325 1330

Leu Ser Leu Ser Pro Gly Lys
1335

SM
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